

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 30, 2002, 11:50:30 ; Search time 27.34 seconds
(without alignments)
72.441 Million cell updates/sec

Title: US-09-432-546-6

Perfect score: 183

Sequence: 1 RRPWWMPKPLIGGGYDPAPPPPP 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 segs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR:68:*

2: PIR:*

3: PIR:*

4: PIR:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 77 | 42.1 | 161 | 2 | E48232 |
| 2 | 71.5 | 39.1 | 248 | 2 | S23449 |
| 3 | 70 | 38.3 | 172 | 2 | T27505 |
| 4 | 68.5 | 37.4 | 221 | 2 | T07176 |
| 5 | 68 | 37.2 | 142 | 2 | T51039 |
| 6 | 68 | 37.2 | 196 | 2 | B48232 |
| 7 | 68 | 37.2 | 209 | 2 | A48232 |
| 8 | 68 | 37.2 | 969 | 2 | T15446 |
| 9 | 66.5 | 36.3 | 160 | 2 | D48232 |
| 10 | 66 | 36.1 | 10 | 2 | A36454 |
| 11 | 66 | 36.1 | 1171 | 2 | T17454 |
| 12 | 65 | 35.5 | 1662 | 2 | T18540 |
| 13 | 64 | 35.0 | 148 | 2 | S39206 |
| 14 | 64 | 35.0 | 534 | 2 | S21961 |
| 15 | 64 | 35.0 | 650 | 2 | T04487 |
| 16 | 64 | 35.0 | 691 | 2 | T46476 |
| 17 | 64 | 35.0 | 1137 | 2 | A86335 |
| 18 | 64 | 35.0 | 1404 | 2 | E85509 |
| 19 | 63 | 34.4 | 172 | 2 | D41132 |
| 20 | 63 | 34.4 | 304 | 2 | A32993 |
| 21 | 62 | 33.9 | 137 | 2 | T23308 |
| 22 | 62 | 33.9 | 144 | 1 | J01222 |
| 23 | 62 | 33.9 | 502 | 2 | T08776 |
| 24 | 62 | 33.9 | 584 | 2 | B84668 |
| 25 | 62 | 33.9 | 776 | 2 | S45495 |
| 26 | 62 | 33.9 | 856 | 2 | T13159 |
| 27 | 61.5 | 33.6 | 445 | 2 | S19990 |
| 28 | 61.5 | 33.6 | 684 | 2 | A56154 |
| 29 | 61 | 33.3 | 106 | 2 | A30996 |

| | | | | | | |
|----|----|------|------|---|--------|--------------------|
| 30 | 61 | 33.3 | 112 | 1 | ASLJX2 | vpu protein - huma |
| 31 | 61 | 33.3 | 112 | 1 | ASLJCX | vpu protein - huma |
| 32 | 61 | 33.3 | 112 | 1 | ASLJST | vpu protein - siml |
| 33 | 61 | 33.3 | 112 | 1 | ASLJX3 | vpu protein - huma |
| 34 | 61 | 33.3 | 112 | 2 | S12155 | gene x protein - h |
| 35 | 61 | 33.3 | 112 | 2 | S03066 | vpx protein - huma |
| 36 | 61 | 33.3 | 112 | 2 | S53094 | vpx protein - h |
| 37 | 61 | 33.3 | 140 | 2 | T19083 | vpx protein - huma |
| 38 | 61 | 33.3 | 249 | 2 | A41497 | hypothetical prote |
| 39 | 61 | 33.3 | 282 | 2 | T26635 | 36k antigen pra - |
| 40 | 61 | 33.3 | 473 | 2 | B85187 | hypothetical prote |
| 41 | 61 | 33.3 | 492 | 2 | T21934 | glycoprotein homol |
| 42 | 61 | 33.3 | 1044 | 2 | S01966 | hypothetical prote |
| 43 | 61 | 33.3 | 1353 | 2 | T19157 | GTPase-activating |
| 44 | 61 | 33.3 | 1424 | 2 | T19156 | probable metal bin |
| 45 | 61 | 33.3 | 1585 | 2 | T31611 | probable metal bin |

ALIGNMENTS

RESULT 1

E48232

Cysteine-rich extensin-like protein 5 precursor - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Nov-2000

C:Accession: E48232

R:Hu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.

Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993

A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich doma

A:Reference number: A48232; MUID:93342083

A:Accession: E48232

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-161 <NUA>

A:Cross-references: GB:L13443; NID:9310930; PID:AAA34063.1; PID:9310931

C:Genetics:

A:Gene: CELP-5

C:Superfamily: glutelin

C:Keywords: cell wall; extracellular matrix; fertilization; glycoprotein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-160/Product: cysteine-rich extensin-like protein 5 #status experimental <MAT>

Query Match

Best Local Similarity 42.1%; Score 77; DB 2; Length 161;

Matches 14; Conservative 2; Mismatches 2; Indels 14; Gaps 3;

QY 3 WFW-----WFW--KWPLIGGGYDPAPPPPP 26

DB 41 WPKIPCYLMPPRPMP-----PSPPPPP 66

RESULT 2

S23449

NMDH oxidase (H2O2-forming) (EC 1.6.-.-) - Thermus aquaticus

C:Species: Thermus aquaticus

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 23-Mar-1993

C:Accession: S23449; S24556

R:Park, H.U.; Kreutzer, R.; Reiser, C.O.A.; Sprinzl, M.

Eur. J. Biochem. 205, 875-879, 1992

A:Title: Molecular cloning and nucleotide sequence of the gene encoding a H(2)O(2)-fo

A:Reference number: S23449; MUID:92245331

A:Accession: S23449

A:Molecule type: DNA

A:Residues: 1-248 <PAR>

A:Cross-references: EMBL:X60110

A:Accession: S24556

A:Molecule type: protein

A:Residues: 1-32 <PAR>

C:Genetics:

A:Gene: nox

C:Keywords: NAD; oxidoreductase

F:1-248/Product: NADH oxidase (H2O2-forming) #status experimental <MAT>

Query Match 39.1%; Score 71.5; DB 2; Length 248;
Best Local Similarity 44.1%; Pred. No. 0.47;
Matches 15; Conservative 0; Mismatches 8; Indels 11; Gaps 3;

OY 1 RRM-----PWWPKWPLIGGGYDPAPPPP 25
Db 167 RSMGFLRPPSPWMPWA-RTTGGCL-PLRPPAP 198

RESULT 3
T27505
hypothetical protein ZC168.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27505

R:Berk, M.
submitted to the EMBL Data Library, March 1996

A:Reference number: Z20378
A:Accession: T27505
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-172 <WLL>
A:Cross-references: EMBL:Z70312; PIDN:CAA94385.1; GSPDB:GN00022; CESP:ZC168.5

C:Genetics:
A:Experimental source: clone ZC168
A:Gene: CESP:ZC168.5
A:Map position: 4
A:introns: 112/3

Query Match 38.3%; Score 70; DB 2; Length 172;
Best Local Similarity 68.8%; Pred. No. 0.46;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 11 PLIGGGYDPAPPPP 26
Db 45 PPGGGGYEAPPPPP 60

RESULT 4

T07176
extensin homolog - potato (fragment)

C:Species: Solanum tuberosum (potato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 17-Nov-2000
C:Accession: T07176

R:MacLeod, M.R.
submitted to the EMBL Data Library, December 1997

A:Reference number: Z15977
A:Accession: T07176
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-221 <MAC>
A:Cross-references: EMBL:AJ003220; NID:el251331; PIDN:CAA06000.1; PID:el251332

A:Experimental source: cv. Record; swelling stolon

C:Superfamily: glutelin

Query Match 37.4%; Score 68.5; DB 2; Length 221;
Best Local Similarity 36.8%; Pred. No. 0.88;
Matches 14; Conservative 3; Mismatches 4; Indels 17; Gaps 3;

OY 3 WPM-----WPKWPLIGGGYD-----PAPPPPP 26
Db 24 WPMWIPCYLWPMFPF---RPYPCPPKRPSPSPPPP 58

RESULT 5

T51039
related to extensin precursor [Imported] - Neurospora crassa
N:Alternate names: protein B15120.90

C:Species: Neurospora crassa

C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000

C:Accession: T51039
R:Schulte, U.; Algin, V.; Hobeisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu

submitted to the Protein Sequence Database, July 2000

A:Reference number: Z25286
A:Accession: T51039

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-142 <SCH>
A:Cross-references: EMBL:AL389900; GSPDB:GN00116; NCSP:B15120.90

A:Experimental source: BAC clone B15120; strain OR74A
C:Genetics:
A:Gene: NCSP:B15120.90
A:Map position: 6

Query Match 37.2%; Score 68; DB 2; Length 142;
Best Local Similarity 42.9%; Pred. No. 0.63;
Matches 15; Conservative 3; Mismatches 7; Indels 10; Gaps 2;

OY 1 RRP-----WPKWPLIG---GGYDPAPPPP 25
Db 87 RRPRLKRPQSWVPKPLTSPFLSPGAPPPP 121

RESULT 6

B48232
cysteine-rich extensin-like protein 2 precursor - common tobacco

C:Species: Nicotiana tabacum (common tobacco)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C:Accession: B48232; PQ0474; S24616

R:Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993

A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
A:Reference number: A48232; M01D:93342083
A:Accession: B48232

A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-196 <WUA>
A:Cross-references: GB:U13440; NID:G310924; PIDN:AAA34060.1; PID:G310925

R:de S. Goldman, M.H.; Pezotli, M.; Seurinck, J.; Mariani, C.
Plant Cell 4, 1041-1051, 1992

A:Title: Developmental expression of tobacco pistil-specific genes encoding novel ext
A:Reference number: PQ0474; M01D:93005740
A:Accession: PQ0474

A:Molecule type: mRNA
A:Residues: 1-105 <GOL>

A:Cross-references: EMBL:Z14014
A:Experimental source: stigma, style; strain Petit Havana SRI
C:Genetics:
A:Gene: CELP-2
A:Superfamily: glutelin

C:Keywords: cell wall; extracellular matrix; fertilization
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-196/Product: cysteine-rich extensin-like protein 2 #status experimental <MAT>

Query Match 37.2%; Score 68; DB 2; Length 196;
Best Local Similarity 38.7%; Pred. No. 0.88;
Matches 12; Conservative 1; Mismatches 2; Indels 16; Gaps 2;

OY 3 WPM-----WPKWPLIGGGYDPAPPPP 26
Db 40 WPMWIPCYLWPMFPF-----PPPP 61

RESULT 7

A48232
cysteine-rich extensin-like protein 1 precursor - common tobacco

C:Species: Nicotiana tabacum (common tobacco)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 01-Dec-2000
C:Accession: A48232; PQ0475; S24617

R;Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993
A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
A:Reference number: A48232; MUID:93342083
A:Accession: A48232
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-209 <MUA>
A:Cross-references: GB:113439; NID:q10922; PIDN:AAA4059.1; PID:q10923
A:de S Goldman, M.H.; Pezotti, M.; Seurinck, J.; Matiani, C.
Plant Cell 4, 1041-1051, 1992
A:Title: Developmental expression of tobacco pistil-specific genes encoding novel extensin
A:Reference number: PQ0474; MUID:93005740
A:Accession: PQ0475
A:Molecule type: mRNA
A:Residues: 39-209 <GOL>
A:Cross-references: GML:214020; NID:q19918; PID:q19919
A:Experimental source: stigma, style; strain Petit Havana SRI
C:Superfamily: glutelin
C:Keywords: cell wall; extracellular matrix; fertilization; glycoprotein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-209/Product: cysteine-rich extensin-like protein 1 #status experimental <MAT>
F:146/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 37.2%; Score 68; DB 2; Length 209;
Best Local Similarity 38.7%; Pred. No. 0.94;
Matches 12; Conservative 1; Mismatches 2; Indels 16; Gaps 2;

OY 3 WPKWPLIGGYDPAAPPPPP 26
DB 45 WPKWPLIGGYDPAAPPPPP 26

RESULT 8
T15446
Hypothetical protein C07G1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15446
R: Hawkins, J.
submitted to the EMBL Data Library, May 1996
A:Description: The sequence of C. elegans cosmid C07G1.
A:Reference number: Z18352
A:Accession: T15446
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-969 <HAM>
A:Cross-references: EMBL:U58751; NID:q1326379; PID:q1326381; PIDN:AA00657.1; GSPDB:GN00
C:Experimental source: strain Bristol N2; clone C07G1
C:Genetics:
A:Gene: CESP:C07G1.4
A:Map position: 4
A:Introns: 110/3; 149/2; 515/1; 564/1; 600/2; 690/2; 755/3; 843/3; 884/3; 940/2

Query Match 37.2%; Score 68; DB 2; Length 969;
Best Local Similarity 35.0%; Pred. No. 4.6;
Matches 11; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 7 WPKWPLIGGYDPAAPPPPP 26
DB 799 WPKWPLIGGYDPAAPPPPP 818

RESULT 9
D48232
cysteine-rich extensin-like protein 4 precursor - common tobacco (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 17-Nov-2000
C:Accession: D48232
R:Wu, H.; Zou, J.; May, B.; Gu, Q.; Cheung, A.Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 6829-6833, 1993

A:Title: A tobacco gene family for flower cell wall proteins with a proline-rich domain
A:Reference number: A48232; MUID:93342083
A:Accession: D48232
A:Status: Preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-160 <MUA>
A:Cross-references: GB:113442
A:Note: authors failed to translate the codon GCT for residue 11 as Ala, and GTA for
A:Note: authors translated the codon TCT for residue 60 as Pro, and CCA for residue 1
C:Genetics:
A:Gene: CELP-4
C:Superfamily: glutelin
C:Keywords: cell wall; extracellular matrix; fertilization; glycoprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-159/Product: cysteine-rich extensin-like protein 4 #status experimental <MAT>

Query Match 36.3%; Score 66.5; DB 2; Length 160;
Best Local Similarity 35.0%; Pred. No. 1;
Matches 14; Conservative 2; Mismatches 5; Indels 19; Gaps 3;

OY 3 WPKWPLIGGYDPAAPPPPP 26
DB 39 WPKWPLIGGYDPAAPPPPP 75

RESULT 10
A36454
trypsin-modulating oostatic factor - yellow fever mosquito
C:Species: Aedes aegypti (yellow fever mosquito)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-May-1996
C:Accession: A36454; A61630
R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
FASEB J. 4, 3015-3020, 1990
A:Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme
A:Reference number: A36454; MUID:90367888
A:Accession: A36454
A:Molecule type: protein
A:Residues: 1-10 <BOR>
R:Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
Insect Biochem. Mol. Biol. 23, 703-712, 1993
A:Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oostatic factor
A:Reference number: A61630; MUID:93357794
A:Accession: A61630
A:Molecule type: protein
A:Residues: 1-10 <BOR>
A:Note: none of the amino acids is modified
C:Function:
A:Description: Inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut
C:Keywords: hormone

Query Match 36.1%; Score 66; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 YDPAPPPPP 26
DB 1 YDPAPPPPP 10

RESULT 11
T17454
diaphanous-related formin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17454
R:Tomimaga, T.; Sahai, E.; Treisman, R.H.; Alberts, A.S.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z18796
A:Accession: T17454
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 1-1171 <TOM>
 A:Cross-references: EMBL:AF094519; NID:g3845724; PID:g3834629; PIDN:AC71771.1
 C:Genetics:
 A:Gene: Diaz

Query Match 36.1%; Score 66; DB 2; Length 1171;
 Best Local Similarity 62.5%; Pred. No. 9.3;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 11 PLIGGYDPAPPPPP 26
 | : | | | | | | | | | |
 Db 559 PALSGGVPPPPPP 574

RESULT 12
 T18540
 moifa protein precursor [imported] - Leptothrix discophora
 C:Species: Leptothrix discophora
 C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 08-Sep-2000
 C:Accession: T18540
 R:Corstjens, P.L.
 submitted to the EMBL Data Library, April 1999
 A:Reference number: Z18959
 A:Accession: T18540
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1662 <COR>
 A:Cross-references: EMBL:Z25774; NID:e1427784; PID:e267517; PIDN:CAA81037.1
 C:Genetics:
 A:Note: moifa
 F1-33/Domain: signal sequence #status predicted <SIG>
 F1-33/Product: moifa protein #status predicted <MAT>

Query Match 35.5%; Score 65; DB 2; Length 1662;
 Best Local Similarity 52.9%; Pred. No. 17;
 Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 QY 2 RMPWMPKMPPLIGGYD 18
 | : | | | | | | | | | |
 Db 490 RMHMGFWFVPFAMVD 506

RESULT 13
 S39206
 proline-rich protein V-beta 1 precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-May-2000
 C:Accession: A53118; S39206
 R:Courtney, Y.; Rosinski-Chupin, I.; Rougeon, F.
 J. Biol. Chem. 269, 520-527, 1994
 A:Title: A new proline-rich protein precursor expressed in the salivary glands of the rat
 A:Reference number: A53118; NID:94103265
 A:Accession: A53118
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-148 <COU>
 A:Cross-references: EMBL:X74229; NID:g433616; PIDN:CAA52300.1; PID:g433617
 A:Note: submitted to the EMBL Data Library, July 1993
 C:Genetics:
 A:Gene: VCS-beta1
 A:Introns: 18/3
 C:Superfamily: proline-rich peptide P-B
 C:Keywords: glycoprotein
 F1-18/Domain: signal sequence #status predicted <SIG>
 F1-18/Product: proline-rich protein V-beta 1 #status predicted <MAT>
 F1-13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 35.0%; Score 64; DB 2; Length 148;
 Best Local Similarity 62.5%; Pred. No. 1.8;
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 11 PLIGGYDPAPPPPP 26
 | : | | | | | | | | | |
 Db 56 PHFGPGFPPPPPP 71

RESULT 14
 S21961
 proline-rich protein ARG - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
 C:Accession: S21961
 R:Roberts, M.R.; Foster, G.D.; Blundell, R.P.; Robinson, S.W.; Draper, J.; Scott, R.J.
 submitted to the EMBL Data Library, August 1991
 A:Description: Cloning and characterization of a proline-rich gene expressed specific
 A:Reference number: S16748
 A:Accession: S21961
 A:Molecule type: DNA
 A:Residues: 1-534 <ROB>
 A:Cross-references: EMBL:X60377; NID:g22598; PID:g22599
 C:Genetics:
 A:Gene: ARG
 A:Introns: 256/1; 299/3; 387/3; 470/1

Query Match 35.0%; Score 64; DB 2; Length 534;
 Best Local Similarity 37.5%; Pred. No. 6.8;
 Matches 12; Conservative 3; Mismatches 11; Indels 6; Gaps 1;
 QY 1 RMPW-----WPKMPPLIGGYDPAPPPPP 26
 | | | | | | | | | | | | | |
 Db 41 RMPWPLMPRPYQPMWPMNPTPDPSPKVPAP 72

RESULT 15
 T04487
 hypothetical protein F8P16.10 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
 R:Bayan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hohenseel, J.; M
 submitted to the Protein Sequence Database, April 1998
 A:Reference number: Z15375
 A:Accession: T04487
 A:Molecule type: DNA
 A:Residues: 1-650 <BEV>
 A:Cross-references: EMBL:AL021633
 A:Experimental source: cultivar Columbia; BAC clone F8P16
 C:Genetics:
 A:Map position: 4
 A:Introns: 337/2; 428/1
 A:Note: F8P16.10

Query Match 35.0%; Score 64; DB 2; Length 650;
 Best Local Similarity 68.8%; Pred. No. 8.3;
 Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 11 PLIGGYDPAPPPPP 26
 | : | | | | | | | | | |
 Db 106 PPFGPYDSAPPPPP 121

Search completed: January 30, 2002, 11:50:31
 Job time: 125 sec

Thu Jan 31 11:07:43 2002

us-09-432-546-6.rpr
